



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/916,808

1/12

Source:

OIPÉ

Date Processed by STIC:

08/08/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 09/916,808

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ Misaligned Amino  
Numbering  
The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☒ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH - Biotechnology Systems Branch - 08/21/2001

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/916,808

DATE: 08/08/2001

TIME: 11:18:55

Input Set : A:\10338\_2U1.txt

Output Set: N:\CRF3\08082001\I916808.raw

Does Not Comply

Corrected Diskette Needed

2 <110> APPLICANT: Gibbs, Mark John  
 3 Gibbs, Adrian John  
 4 Brown, Roger William  
 6 <120> TITLE OF INVENTION: Combinatorial probes and uses therefor  
 8 <130> FILE REFERENCE: 10338-2U1  
 10 <140> CURRENT APPLICATION NUMBER: US/09/916,808  
 11 <141> CURRENT FILING DATE: 2001-07-27  
 13 <150> PRIOR APPLICATION NUMBER: AU PQ9026/00  
 14 <151> PRIOR FILING DATE: 2000-07-27  
 16 <150> PRIOR APPLICATION NUMBER: AU PQ9483/00  
 17 <151> PRIOR FILING DATE: 2000-08-17  
 19 <150> PRIOR APPLICATION NUMBER: US 60/226212  
 20 <151> PRIOR FILING DATE: 2000-08-18  
 22 <160> NUMBER OF SEQ ID NOS: 26  
 24 <170> SOFTWARE: PatentIn version 3.1  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 10  
 28 <212> TYPE: DNA  
 29 <213> ORGANISM: Synthetic  
 31 <400> SEQUENCE: 1  
 32 agctcattga 10  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 9  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Synthetic  
 40 <400> SEQUENCE: 2  
 41 agctcattg 9  
 44 <210> SEQ ID NO: 3  
 45 <211> LENGTH: 9  
 46 <212> TYPE: DNA  
 47 <213> ORGANISM: Synthetic  
 49 <400> SEQUENCE: 3  
 50 gctcattga 9  
 53 <210> SEQ ID NO: 4  
 54 <211> LENGTH: 8  
 55 <212> TYPE: DNA  
 56 <213> ORGANISM: Synthetic  
 58 <400> SEQUENCE: 4  
 59 agctcatt 8  
 62 <210> SEQ ID NO: 5  
 63 <211> LENGTH: 8  
 64 <212> TYPE: DNA  
 65 <213> ORGANISM: Synthetic  
 67 <400> SEQUENCE: 5  
 68 gctcattg 8  
 71 <210> SEQ ID NO: 6  
 72 <211> LENGTH: 8

The types of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/916,808

DATE: 08/08/2001  
TIME: 11:18:55

Input Set : A:\10338\_2U1.txt  
Output Set: N:\CRF3\08082001\I916808.raw

73 <212> TYPE: DNA  
74 <213> ORGANISM: Synthetic  
76 <400> SEQUENCE: 6  
77 ctcatgga 8  
80 <210> SEQ ID NO: 7  
81 <211> LENGTH: 20  
82 <212> TYPE: DNA  
83 <213> ORGANISM: Synthetic  
85 <220> FEATURE:  
86 <221> NAME/KEY: misc\_feature  
87 <222> LOCATION: (3)..(3)  
88 <223> OTHER INFORMATION: n=g, a, c or t *OK*  
91 <220> FEATURE:  
92 <221> NAME/KEY: misc\_feature  
93 <222> LOCATION: (15)..(15)  
94 <223> OTHER INFORMATION: n=g, a, c or t  
97 <400> SEQUENCE: 7  
W--> 98 ggnaayaaya gyggncarcc *6* 20  
101 <210> SEQ ID NO: 8  
102 <211> LENGTH: 15  
103 <212> TYPE: DNA  
104 <213> ORGANISM: Synthetic *Errored*  
106 <400> SEQUENCE: 8  
107 ggaaaacagg gcacc 15  
110 <210> SEQ ID NO: 9  
111 <211> LENGTH: 15  
112 <212> TYPE: DNA  
113 <213> ORGANISM: Synthetic  
115 <400> SEQUENCE: 9  
116 ggaaaatagg gcacc 15  
119 <210> SEQ ID NO: 10  
120 <211> LENGTH: 15  
121 <212> TYPE: DNA  
122 <213> ORGANISM: Synthetic  
124 <400> SEQUENCE: 10  
125 gggaaaaagg gcacc 15  
128 <210> SEQ ID NO: 11  
129 <211> LENGTH: 15  
130 <212> TYPE: DNA  
131 <213> ORGANISM: Synthetic  
133 <400> SEQUENCE: 11  
134 ggaaaaaagg gcacc 15  
137 <210> SEQ ID NO: 12  
138 <211> LENGTH: 15  
139 <212> TYPE: DNA  
140 <213> ORGANISM: Synthetic  
142 <400> SEQUENCE: 12  
143 ggcaaaaagg gcacc 15  
146 <210> SEQ ID NO: 13

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PATENT APPLICATION: US/09/916,808

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Input Set : A:\10338\_2U1.txt

Output Set: N:\CRF3\08082001\I916808.raw

```

147 <211> LENGTH: 15
148 <212> TYPE: DNA
149 <213> ORGANISM: Synthetic
151 <400> SEQUENCE: 13
152 ggtaaaaagg gcacc 15
155 <210> SEQ ID NO: 14
156 <211> LENGTH: 15
157 <212> TYPE: DNA
158 <213> ORGANISM: Synthetic
160 <400> SEQUENCE: 14
161 ggaacaaagg gcacc 15
164 <210> SEQ ID NO: 15
165 <211> LENGTH: 15
166 <212> TYPE: DNA
167 <213> ORGANISM: Synthetic Eroneel
169 <400> SEQUENCE: 15
170 ggaataaagg gcacc 15
173 <210> SEQ ID NO: 16
174 <211> LENGTH: 20
175 <212> TYPE: DNA
176 <213> ORGANISM: Synthetic
178 <400> SEQUENCE: 16
179 gggaacaaca gcgggcaacc 20
182 <210> SEQ ID NO: 17
183 <211> LENGTH: 14
184 <212> TYPE: DNA
185 <213> ORGANISM: Synthetic
187 <220> FEATURE:
188 <221> NAME/KEY: misc_feature
189 <222> LOCATION: (3)..(3)
190 <223> OTHER INFORMATION: n=g, a, c or t
193 <400> SEQUENCE: 17
W--> 194 ggnaayaaya gygg 14
197 <210> SEQ ID NO: 18
198 <211> LENGTH: 17
199 <212> TYPE: DNA
200 <213> ORGANISM: Synthetic
202 <220> FEATURE:
203 <221> NAME/KEY: misc_feature
204 <222> LOCATION: (12)..(12) ok
205 <223> OTHER INFORMATION: n=g, a, c or t
208 <400> SEQUENCE: 18
W--> 209 aayaayagy gncarcc 17
212 <210> SEQ ID NO: 19
213 <211> LENGTH: 20
214 <212> TYPE: DNA
215 <213> ORGANISM: Synthetic
217 <400> SEQUENCE: 19
218 gggaacaaca gcgggcaacc 20

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/916,808

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TIME: 11:18:55

Input Set : A:\10338\_2U1.txt

Output Set: N:\CRF3\08082001\I916808.raw

```

221 <210> SEQ ID NO: 20
222 <211> LENGTH: 11
223 <212> TYPE: DNA
224 <213> ORGANISM: Synthetic
226 <220> FEATURE:
227 <221> NAME/KEY: misc_feature
228 <222> LOCATION: (3)..(3)
229 <223> OTHER INFORMATION: n=g, a, c or t
232 <400> SEQUENCE: 20
W--> 233 ggnaayaaya g 11
236 <210> SEQ ID NO: 21
237 <211> LENGTH: 11
238 <212> TYPE: DNA
239 <213> ORGANISM: Synthetic
241 <400> SEQUENCE: 21
242 aayaayagyg g 11
245 <210> SEQ ID NO: 22
246 <211> LENGTH: 11
247 <212> TYPE: DNA
248 <213> ORGANISM: Synthetic
250 <220> FEATURE:
251 <221> NAME/KEY: misc_feature
252 <222> LOCATION: (6)..(6)
253 <223> OTHER INFORMATION: n=g, a, c or t
256 <400> SEQUENCE: 22
W--> 257 agyggncarc c 11
260 <210> SEQ ID NO: 23
261 <211> LENGTH: 16
262 <212> TYPE: DNA
263 <213> ORGANISM: Synthetic
265 <220> FEATURE:
266 <221> NAME/KEY: misc_feature
267 <222> LOCATION: (8)..(8)
268 <223> OTHER INFORMATION: n=g, a, c or t
271 <400> SEQUENCE: 23
W--> 272 ggtgyatnga vaaygg 16
275 <210> SEQ ID NO: 24
276 <211> LENGTH: 13
277 <212> TYPE: DNA
278 <213> ORGANISM: Synthetic
280 <220> FEATURE:
281 <221> NAME/KEY: misc_feature
282 <222> LOCATION: (8)..(8)
283 <223> OTHER INFORMATION: n=g, a, c or t
286 <400> SEQUENCE: 24
W--> 287 ggtgyatnga vaa 13
290 <210> SEQ ID NO: 25
291 <211> LENGTH: 11
292 <212> TYPE: DNA

```

RAW SEQUENCE LISTING  
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DATE: 08/08/2001  
TIME: 11:18:55

Input Set : A:\10338\_2U1.txt  
Output Set: N:\CRF3\08082001\I916808.raw

293 <213> ORGANISM: Synthetic  
295 <220> FEATURE:  
296 <221> NAME/KEY: misc\_feature  
297 <222> LOCATION: (3)..(3)  
298 <223> OTHER INFORMATION: n=g, a, c or t  
301 <400> SEQUENCE: 25  
W--> 302 atngavaayg g 11  
305 <210> SEQ ID NO: 26  
306 <211> LENGTH: 12  
307 <212> TYPE: DNA  
308 <213> ORGANISM: Synthetic  
310 <220> FEATURE:  
311 <221> NAME/KEY: misc\_feature  
312 <222> LOCATION: (9)..(9)  
313 <223> OTHER INFORMATION: n=g, a, c or t  
316 <400> SEQUENCE: 26  
W--> 317 aaygadgtng ay 12

VERIFICATION SUMMARY  
PATENT APPLICATION: US/09/916,808

DATE: 08/08/2001  
TIME: 11:18:56

Input Set : A:\10338\_2U1.txt  
Output Set: N:\CRF3\08082001\I916808.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7  
L:194 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
L:233 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
L:257 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22  
L:272 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24  
L:302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25  
L:317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26